

Amendments to the Specification

Please replace the second full paragraph on page 32 with the following amended paragraph:

These and other embodiments are disclosed or are obvious from and encompassed by the description and examples of the present invention. Further literature concerning any one of the methods, uses and compounds to be employed in accordance with the present invention may be retrieved from public libraries, using for example electronic devices. For example the public database "Medline" may be utilized which is available on the Internet, e.g. under ~~<http://www.ncbi.nlm.nih.gov/PubMed/medline.html>~~. Further databases and addresses, such as ~~<http://www.ncbi.nlm.nih.gov/>, <http://www.infobiogen.fr/>, http://www.fmi.ch/biology/research_tools.html, <http://www.tigr.org/>~~, are known to the person skilled in the art and can also be obtained using, e.g., ~~<http://www.lycos.com>~~ the PubMed website, the NCBI website, the InfoBiogen website, the Institute for Genomic Research (TIGR) website, and the lycos website. An overview of patent information in biotechnology and a survey of relevant sources of patent information useful for retrospective searching and for current awareness is given in Berks, TIBTECH 12 (1994), 352-364.

Please replace Table 1 on page 39 with the following amended Table 1:

| Name | Position | Sequence (5' - 3') | <u>Sequence Identifier</u> |
|-------|----------|----------------------|----------------------------|
| T7 | BAC CS | TAATACGACTCACTATAGGG | <u>SEQ ID NO:1</u> |
| 3A43F | exon 2 | GAACCCATTCACATGGAC | <u>SEQ ID NO:2</u> |
| 3A46R | exon 4 | TGATCATGTCAGGATCTG | <u>SEQ ID NO:3</u> |

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| | | | |
|----------|-----------|--------------------------|---------------------|
| 3A47F | exon 4 | GGTCAACAGCCTGTGCTG | <u>SEQ ID NO:4</u> |
| 3A48R | exon 5 | TCCACTGGTGAAGGTTGG | <u>SEQ ID NO:5</u> |
| 3A49F | exon 5 | GTGCCATCTCTATAGCTG | <u>SEQ ID NO:6</u> |
| 3A410R | exon 6 | CTTCCCGCCTCAGATTC | <u>SEQ ID NO:7</u> |
| 3A411F | exon 6 | GAAATCTGAGGCGGGAAG | <u>SEQ ID NO:8</u> |
| 3A412R | exon 7 | GGGTCTTGTGGATTGTTG | <u>SEQ ID NO:9</u> |
| 3A413F | exon 7 | CAACAATCCACAAGACCC | <u>SEQ ID NO:10</u> |
| 3A414R | exon 8 | GTGTATCTTCGAGGCGAC | <u>SEQ ID NO:11</u> |
| 3A415F | exon 8 | CTTCCATTCCTCATCCC | <u>SEQ ID NO:12</u> |
| 3A416R | exon 9 | CCTTTGTGGGACTCAGTTTC | <u>SEQ ID NO:13</u> |
| 3A419F | exon 10 | GCCACTCACCTGATGTC | <u>SEQ ID NO:14</u> |
| 3A720R | exon 11 | ATCACCAACCCACCCTTG | <u>SEQ ID NO:15</u> |
| 3A721F | exon 11 | CAAAGGGTGGGTGGTGAT | <u>SEQ ID NO:16</u> |
| 3A422R | exon 12 | GAGAGCAAACCTCATGCC | <u>SEQ ID NO:17</u> |
| 3A423F | exon 12 | GGCATGAGGTTTGCTCTC | <u>SEQ ID NO:18</u> |
| 3A424R | exon 13 | GGTGCCATCCCTTGACTC | <u>SEQ ID NO:19</u> |
| 3A426R | exon 2 | GCAGAGGTGTGGGCCCTG | <u>SEQ ID NO:20</u> |
| 3A4436F | intron 8 | GGAGATCAAGGACCACGCTTGTG | <u>SEQ ID NO:21</u> |
| 3A441R | intron 10 | CTTACGCTTCTGCCAGTAGCAACC | <u>SEQ ID NO:22</u> |
| CYP3A4PF | promoter | AACAGGCGTGGAACACAAT | <u>SEQ ID NO:23</u> |
| CYP3A4PR | promoter | CTTTCCTGCCCTGCACAG | <u>SEQ ID NO:24</u> |

Please replace Table 2 on page 41 with the following amended Table 2:

| Exon | Primer name | Primer sequence (5' - 3' orientation) | Location on BAC 22300 | Fragment length | Annealing Temp. | SEQ ID NO: |
|----------------|----------------------|---------------------------------------|-----------------------|-----------------|-----------------|------------|
| 1 | 3 ^a 4-62F | AACTGCAGGCAGAGCACAGGT | 61838 - 61858 | 384 bp | 63°C | <u>25</u> |
| | 3A4-64R | CCACGCCCCGGCCTGAACATCT | 62221 - 62201 | | | <u>26</u> |
| 2 ^a | 3A4-101F | TAGGATCCAATCATCTCCTAC | 65072 - 65092 | 463 bp | 62°C | <u>27</u> |
| | 3A4-68F | GGTGTCTCATGGTGGAGG | 65841 - 65858 | | | <u>28</u> |
| | 3A4-103R | AGAGTTAGCAAGAGAGCCCTT | 66303 - 66283 | | | <u>29</u> |

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| | | | | | | |
|----------------|----------|------------------------------------|---------------|--------|------|------------|
| 3 | 3A4-50F | CCTCTAACTGCCAGCAAGTCTG | 67924 - 67945 | 249 bp | 58°C | <u>30</u> |
| | 3A4-51R | GCGCTGAGACTGTCCTCTGTG | 68172 - 68152 | | | <u>31</u> |
| 4 ^b | 3A4-52F | AGTCTGGCTTCCTGGGTTGGGCTC | 73343 - 73366 | 293 bp | 58°C | <u>32</u> |
| | 3A4-37R | GAAGTGGACGTGGAACCTTCCTGGAC | 73635 - 73610 | | | <u>142</u> |
| | 3A4-100R | GGGGACAGGATGAAGTGGACG | 73646 - 73626 | 304 bp | 63°C | <u>33</u> |
| 5 | 3A4-28F | TACAACCATGGAGACCTCC | 75813 - 75832 | 236 bp | 62°C | <u>34</u> |
| | 3A4-29R | TACCTGTCCCCACCAGATTC | 76048 - 76029 | | | <u>35</u> |
| 6 | 3A4-57F | CCCTTTCCAAGGGGTAGTCC | 76066 - 76085 | 379 bp | 58°C | <u>36</u> |
| | 3A4-32R | GTCTGGTCACTGGAATAACCCAACAGC AGG | 76444 - 76415 | | | <u>37</u> |
| 7 | 3A4-33F | GTCTGTCTTGACTGGACATGTGG | 77509 - 77531 | 393 bp | 58°C | <u>38</u> |
| | 3A4-34R | GATGATGGTCACACATATCTTC | 77901 - 77880 | | | <u>39</u> |
| 8 | 3A4-35F | GGCTTCCAGTTGAGAACCTTGATGTC | 78723 - 78748 | 389 bp | 58°C | <u>40</u> |
| | 3A4-59R | GCTCTAAACATGAGCAGTCTTC | 79111 - 79090 | | | <u>41</u> |
| 9 | 3A4-36F | GGAGATCAAGGACCACGCTTGTC | 79584 - 79606 | 240 bp | 62°C | <u>42</u> |
| | 3A4-47R | CTCATCATCCTGGAATACTTCCTGC | 79823 - 79799 | | | <u>43</u> |
| 10 | 3A4-82F | CCCAGTGACCTCTGAATTGC | 81959 - 81979 | 431 bp | 50°C | <u>44</u> |
| | 3A4-95R | CAGAGCCTTCCTACATAG | 82389 - 82372 | | | <u>45</u> |
| 11 | 3A4-97F | CAGTATGAGTTAGTCTCTGG | 83733 - 83752 | 574 bp | 50°C | <u>46</u> |
| | 3A4-80R | CATAACTGATGACCTTCATCG | 84306 - 84286 | | | <u>47</u> |
| 12 | 3A4-49F | CCTGTGTACTGCTAGTAGAGGG | 85020 - 85041 | 411 bp | 50°C | <u>48</u> |
| | 3A4-39R | CACAGATGGGCCTAATTG | 85430 - 85413 | | | <u>49</u> |
| 13 | 3A4-48F | GGAGTGTCTCACTCACTTTGATGC | 87799 - 87822 | 288 bp | 50°C | <u>50</u> |
| | 3A4-25R | TGGATGAAGCCCATCTTC | 88086 - 88069 | | | <u>51</u> |
| 11 | 3A7-42F | CCAGTATGAGTTGTTCTCTGG | 87799 - 87822 | 404 bp | 58°C | <u>140</u> |
| | 3A7-38R | AGGCAGAATATGCTTGAACCAGGC | 88086 - 88069 | | | <u>141</u> |

Please replace Table 3 on page 43 with the following amended Table 3:

| Nr | Variant ^b | Nucleotide sequence (5'-3') | Genetic element | Predicted effect | N ^c | Heterozygotes found (%) | Homozygotes found (%) | Homozygotes calculated (%) | Variant allele frequency (%) | SEQ ID NO: (* = reverse complement) |
|-----|----------------------|--------------------------------|-----------------|------------------|----------------|-------------------------|-----------------------|----------------------------|------------------------------|-------------------------------------|
| M1 | g.6004G>A | TCCCAGGGCTTTTGTA..... | Exon 3 | G56D | 426 | 2,82 | 0,00 | 0,0190 | 1,41 | 52 54 53 55 |
| M2 | g.13908G>A | ATTACGATCATA..... | Exon 5 | R130Q | 300 | 0,66 | 0,00 | 0,0011 | 0,33 | 60 62 61 63 |
| M3 | g.14292G>A | AGCCTGTCACCA..... | Exon 6 | V170I | 424 | 0,47 | 0,00 | 0,0006 | 0,24 | 64 66 65 67 |
| M4 | g.14304G>C | TGAAACACGTAAG..... | Exon 6 | D174H | 424 | 0,47 | 0,00 | 0,0006 | 0,24 | 68 70 69 71 |
| M10 | g.14323C>T | GCAGCCATGGGT..... | Intron 6 | | 424 | 0,47 | 0,00 | 0,0006 | 0,24 | 72 74 73 75 |
| M11 | g.14329G>T | ATGGGGTTCTGT..... | Intron 6 | | 424 | 0,47 | 0,00 | 0,0006 | 0,24 | 76 78 77 79 |
| M12 | g.14357T>G | CCAGCTGCCTGG..... | Intron 6 | | 424 | 1,89 | 0,00 | 0,009 | 0,94 | 80 82 81 83 |
| M13 | g.15753T>G | TATCTTTCTCTCTTG..... | Intron 7 | | 296 | 5,41 | 0,00 | 0,073 | 2,70 | 56 58 57 59 |
| M14 | g.20230G>A | GGATGGTACATA..... | Intron 10 | | 296 | 17,56 | 0,68 | 0,895 | 9,46 | 84 86 85 87 |
| M5 | g.21867C>T | TGAAACGCTCAT..... | Exon 11 | T363M | 298 | 0,67 | 0,00 | 0,001 | 0,34 | 88 90 89 91 |
| M15 | g.21868G>A | GAAACGCTCAGA..... | Exon 11 | Silent | 298 | 0,67 | 0,00 | 0,001 | 0,34 | 92 94 93 95 |
| M6 | g.21896C>T | TGAGACTTGAGT..... | Exon 11 | L373F | 298 | 0,67 | 0,00 | 0,001 | 0,34 | 96 98 97 99 |
| M7 | g.22026C>T | CCTCCCTGAAAT..... | Exon 11 | P416L | 298 | 0,67 | 0,00 | 0,001 | 0,34 | 100 102 101 103 |
| M16 | g.22041C>T | CAAGGCCCTCGT..... | Intron 11 | | 298 | 0,67 | 0,00 | 0,001 | 0,34 | 104 106 105 109 |
| M17 | g.23081C>T | ACCAACGTGGAT..... | Intron 11 | | 426 | 0,47 | 0,00 | 0,001 | 0,23 | 108 110 107 111 |
| M8 | g.23172T>C | TGGCATGAGGTC..... | Exon 12 | M445T | 426 | 0,94 | 0,00 | 0,002 | 0,47 | 112 114 113 115 |
| M18 | g.25925C>T | GGCACCGTAAGT..... | Exon 13 | Silent | 300 | 0,66 | 0,00 | 0,001 | 0,33 | 116 118 112 119 |
| M19 | g.25958T>G | ACTTCTGCTTTG..... | 3'UTR | | 300 | 0,66 | 0,00 | 0,001 | 0,33 | 120 122 121 123 |